



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

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(E) COUNTRY: United Kingdom  
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(ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR  
SEX IDENTIFICATION IN BIRDS

(iii) NUMBER OF SEQUENCES: 41

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/GB96/01341  
(B) FILING DATE: 05-JUN-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511439.3  
(B) FILING DATE: 06-JUN-1995

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(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CCCGGTCGGA GGTTC AAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC      60
AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT      120
AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTGA GCGAAGTTG TTTGGGGATT      180
TTAGTTTGGT TTCCCTGTCA CTGTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG      240
AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA      300
CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG      360
ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC      420
ATTAATTGCT TGTTTTATGA AACCACCTCT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA      480
TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG      540
ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT      600
CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA      660
GTTGTGTGTT TGAGGAAAAA TAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC      720
GGG                                                                    723
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
ATTCTTCCAG ATGATCCTGA TAAAAACCA CAAGCAAAC AGTTACAGAC CAAAAACCA      60
```

CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT 120  
 GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG 153

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC 60  
 CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT 120  
 GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC 60  
 CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
 GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA 60  
CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT 120  
GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA 153

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
1 5 10 15  
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys  
20 25 30  
Arg Glu Ala Gln Arg Leu Cys Gly Ala  
35 40

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
1 5 10 15  
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
20 25 30  
Lys Glu Ala Gln Arg Leu Ala Gly Ala  
35 40

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
1                  5                  10                  15  
  
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
                  20                  25                  30  
  
Lys Glu Ala Gln Arg Leu Ala Gly Ala  
                  35                  40

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln  
1                  5                  10                  15  
  
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg  
                  20                  25                  30  
  
Lys Glu Val Gln Arg Leu Thr Gly Ala  
                  35                  40

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6608 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC	60
CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG	120
CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC	180
ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA	240
GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG	300
GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA	360
GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG	420
AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT	480
CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA	540
AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA	600
GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAACTAA GAAGAAAAAG CATAAAGATG	660
AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG	720
CGGAAGATGG GGATAAAGC AGTTGTGAAG AAAGTGAATC TGAATATGAG CCAAAAAACA	780
AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG	840
GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG	900
ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA	960
CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG	1020
AAGATGAATT TGAACTATA GAGAAGTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA	1080
CTGGTGCCCTC AACCACCATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG	1140
AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA	1200
TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA	1260
AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC	1320
CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT	1380
ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG	1440
ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC	1500

TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
CTACTCCCTT	TAAGGACTGC	AAGGTTCTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
TGGGTCTGGG	TAAAACAATA	CAAACAATTT	CTTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
AACTGTATGG	CCCTTTTCTT	CTGCGCGTGC	CACTTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTTA	CTTAGGAGAT	ATAACTAGTA	1920
GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTTAAAC	1980
TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCCTTGGT	GGTCTCAATT	2040
GGGCATTTCAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
ATTCCCTCAA	AGAGCTGTGG	TCTTTGTTGC	ATTCATCAT	GCCAGAAAAA	TTTTCCTCCT	2220
GGGAAGATTT	TGAAGAGGAG	CATGGCAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
AAGAGCTTGA	ACCATTTTTA	CTAAGAAGAG	TTAAAAAGA	TGTAGAAAAG	TCTTTACCTG	2340
CTAAGGTTGA	ACAAATTCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
GGATTTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTTT	AAAAGGCAGT	ACCTCAGGCT	2460
TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520
CAGATGATAA	TGAATTCTAT	AATAAACAGG	AGGCCTTACA	GCATTTGATA	CGTAGCAGCG	2580
GGAAACTAAT	CCTTCTTGAC	AAGCTACTGA	TTCGTCTGCG	AGAACGTGGC	AACAGAGTTC	2640
TGATTTTCTC	TCAGATGGTG	AGGATGCTGG	ACATCCTAGC	AGAATATCTG	AAGTATCGCC	2700
AGTTTCCCTT	CCAGAGACTT	GATGGATCAA	TAAAAGGGGA	ATTGAGGAAG	CAAGCACTGG	2760
ATCATTTCAA	TGCAGAAGGA	TCAGAGGATT	TCTGTTTTTT	ACTGTCTACA	AGAGCTGGAG	2820
GATTAGGTAT	TAACTTGGA	TCTGCTGACA	CTGTAGTTAT	TTTTGATTCT	GACTGGAATC	2880
CACAGAATGA	TCTGCAGGCA	CAGGCGAGAG	CTCATAGAAT	TGGACAGAAG	AAACAGGTTA	2940
ATATTTATCG	GCTAGTCACA	AAAGGATCAG	TAGAAGAAGA	TATTCTTGAA	AGAGCCAAGA	3000
AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA	AAAACGTGTC	3060
TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTTAA	TAAAGAAGAG	TTATCAGCTA	3120
TTTTGAAGTT	TGGTGCTGAG	GAAGCTTTTA	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	3180
AGGAAATGGA	TATAGATGAA	ATCTTGAAGA	GAGCTGAAAC	TCGGGAAAAT	GAGCCAGGTC	3240

CATTGACTGT AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG	3300
ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAG AAATTGGGAA GAAATCATCC	3360
CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT	3420
ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA	3480
GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC	3540
GGCCAAAAAA GCGTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG	3600
ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT	3660
TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC TGAGACAGAC CTTAGACGTT	3720
TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG	3780
AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC	3840
AGGTGAATGC AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACTG CACAAATCCA	3900
TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC	3960
ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT	4020
ATGGCTATGG CAGCTGGGAA ATGATAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA	4080
TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT	4140
ACCTCATTA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG	4200
CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG GCTTCAAAAA	4260
TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCTC AGAAAAATCT GATGAAGATG	4320
ATGAGGAGGA GGATAACAAG GTAAATGAAA TGAAATCTGA AAATAAAGAA AAATCTAAAA	4380
AAATTCCATT GCTGGATACT CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT	4440
CAGAAGAATC TGAAGAACTC CATCAGAAGA CATTTAGTGT GTGCAAAGAA AGAATGAGGC	4500
CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGCCTTTCT GAAAGGGAGC	4560
AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA TCACATTACA GAATGCCTGA	4620
AGGAGTACAC AAATCCCGAG CAAATAAAAC AGTGGAGGAA AAATTTGTGG ATTTTGTGT	4680
CCAAGTTTAC AGAATTTGAT GCCAGAAAGC TGCACAACT CTACAAACAT GCAATCAAAA	4740
AGCGCCAAGA GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG	4800
TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT GATAGTAGCA	4860
GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA TGATCATCAC AAAGACAGGC	4920



ATCAGGGAGA TGCTTACAAG AAAAGTGACT CCAGGAAAAG GCCATATTCA GCCTTCAGTA	4980
ATGGAAAAGA TCACAGAGAC TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA	5040
GTAAACATAG AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA	5100
ACTTAAAAGA CAGCCGGGGT CATTGAGATC ACCGCTCCCA TTCAGACCAC AGGATACACT	5160
CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC TTCGAGAGAT TATAGATACC	5220
ACTCAGACTG GCAAATGGAC CACAGAGCTT CTGGTAGTGG CCCGAGGTCA CCACTAGATC	5280
AGAGGTCTCC TTATGGTTCA AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT	5340
CAGATCACAA AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA	5400
CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAACTA ACACAGTAAT TGCCTTACAT	5460
GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT ATTGTTACTT CTTTCCAGGA	5520
TGCAAGGTCT ATTATCCCAA CAGAAGAAAA ATATTTTGTG ATTTAAAGTT TATGCTGCAC	5580
TGTGCTGCAA ATGTTGTGGC ACTTTTTTTT TAAGAAATGG AAGATGTTA CTTTACAGG	5640
GACCTCAACA CTGCCCCTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG	5700
TTCTAGGCTG AACACAGATT AAATTATGTT TGTAAATGAA CACTTAAACA CTGACCTGTG	5760
CTTATGTTTC AGGAAAGAAT GGGGGATTTA TTTTGTTTTA TTTCTTGGTA GAGAACTCTC	5820
AAGGACTTTG TTCACTTTC AAAGCTACTT GTTTACATTG TACACTGCGA CCACCTTGCC	5880
GCTTTTCATC ACAAGCTTGA ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA	5940
TTTCTCCTGT TTGTGATCAG TTATAATGCC TTTTATGAA ACAAACAAAC AAACAAAAAA	6000
CAATTAAAAA AAAAAACACA ACAAACCAA CAAATGGCTG TAAATTATTG TAAATTAATT	6060
AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTCTT TTCCCAACA ACTCAGGCCT	6120
TCTTTTCACA AAGTCAGTAT ACTTACATGT TTTAATAAAA TATCTCGATG GAATCAGAAT	6180
GTAAAAATGG GGAAGGGAAT ATTTTATTC ATTTAGTGCT CCTTTTTTAT TGGATACTTT	6240
TACATACCTG TTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAACT GTGAGTGTG	6300
TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG AAAGCTTTTC	6360
AGGTGCATTG GTTTAAAAGA AGGAAGTGTT CTATAGTGTA ACACTCAAA ACCCAGATCA	6420
GCCAAGATTC ATTGTAAATC CATTTGTTTT CCCTCTTTAA CATGGGCAAT AATGTCAAAT	6480
GTGCTATGCA GCAGTTAATA TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC	6540
AATGCACACT GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA	6600
AAAAAACC	6608

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Asp Glu Ile Val Ser Val Lys His Leu His Lys Lys Ile Lys Thr Glu
1           5           10           15
Lys Glu Asn Glu Glu Lys Pro Glu Pro Asp Ile Gly Ile Lys Lys Glu
20          25          30
Ala Glu Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys Arg Glu Leu
35          40          45
Lys Arg Glu Lys Lys Glu Lys Glu Asp Lys Lys Glu Leu Lys Glu Lys
50          55          60
Asp Asn Lys Glu Lys Arg Glu Asn Lys Val Lys Glu Ser Thr Gln Lys
65          70          75          80
Glu Lys Glu Val Lys Glu Glu Lys
85
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
GATGAGATTG TTTCAGTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA      60
AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA      120
AGAGAAGGAA AATAAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAAGAGG ATAAGAAAGA      180
ATTAAAAGAA AAAGATAATA AAGAAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA      240
```

## (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

GATGGGATTG TTTCAGTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA      60
AGAAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA      120
AGAAAAGGAA AATAAGA                                     137

```

## (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu
1           5           10           15
Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu
20           25           30
Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys
35           40           45

```

## (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA	60
AAGATGGTGT TAGATCATTT AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA	120
CATACAGGCT CTA CTCTCCTTC AAGCTCAACA CCTTTTAATA AGGAAGAGTT ATCAGCAATT	180
TTGAAGTTTG GTGCTGAGGA ACTTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG	240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAACTC GAGAAAATGA GTCAGGCCCA	300
TTAACTGTAG GAGATGAGTT ACTTTTCACAG TTCAAGGTAG CTA ACTTTTC CAATATGGAT	360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGAAGA AATCATTCCA	420
GAAGTTCAGT GGCACGAAT AGAGGGGNG GAAAGACAAA AAGAACTTGA AGAAATATAT	480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA	540
TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA	600
CCAAAAAAC GTGGACGACC ACGAACTATT CCCCCTGAAA ACATTAAAGG ATTTAGTGAT	660
GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGCCCAGT TGAAAGGTTA	720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGCTG	780
GGAGAACTTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA	840
AGAACAGGTG GTAGATTTGG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG	900
GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT	960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT	1020
TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT	1080
GGTTATGGCA GTTGGGAAAT GATAAAATG GATCCTGATC TCAGTTTGAC ACAGAAGATT	1140
TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC	1200
CTCATTAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA	1260
GGCAATTCAA AGAGGAGAAA AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC	1316

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala  
1 5 10 15  
Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile  
20 25 30  
Leu Asp Leu His Leu Val Thr Val Asp Phe Leu Phe Asn Phe Leu Ile  
35 40 45  
Leu Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn Ser Ser  
50 55 60  
Gly Glu Ser Ser Arg Ser Asp Asp Asp Ser Ala Gly Ser Ala Ser Gly  
65 70 75 80  
Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser Ser  
85 90 95  
Gln Ser Gly Ser Ser Asp Ser Glu Ser Gly Ser Glu Ser Gly Ser Gln  
100 105 110  
Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Lys Lys Gln Val Gln Ala  
115 120 125  
Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser  
130 135 140  
Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln Gln  
145 150 155 160  
Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser  
165 170 175  
Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys  
180 185 190  
His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly  
195 200 205  
Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys  
210 215 220  
Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg  
225 230 235 240  
Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly  
245 250 255  
Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Glu Asp Asp Asp  
260 265 270

Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val  
 275 280 285  
 Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu  
 290 295 300  
 Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu  
 305 310 315 320  
 Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr  
 325 330 335  
 Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn  
 340 345 350  
 Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile  
 355 360 365  
 Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu  
 370 375 380  
 Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr  
 385 390 395 400  
 Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro  
 405 410 415  
 Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu  
 420 425 430  
 His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln  
 435 440 445  
 Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu  
 450 455 460  
 Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys  
 465 470 475 480  
 Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr  
 485 490 495  
 Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val  
 500 505 510  
 Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu  
 515 520 525  
 Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp  
 530 535 540  
 Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys  
 545 550 555 560  
 Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln  
 565 570 575

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser  
 580 585 590  
 Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val  
 595 600 605  
 Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp  
 610 615 620  
 Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr  
 625 630 635 640  
 Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp  
 645 650 655  
 Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser  
 660 665 670  
 Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu  
 675 680 685  
 Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu  
 690 695 700  
 Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu  
 705 710 715 720  
 Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys  
 725 730 735  
 Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys  
 740 745 750  
 Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala  
 755 760 765  
 Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala  
 770 775 780  
 Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met  
 785 790 795 800  
 Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro  
 805 810 815  
 Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile  
 820 825 830  
 Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu  
 835 840 845  
 Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met  
 850 855 860  
 Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln  
 865 870 875 880

Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp  
 885 890 895  
 His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr  
 900 905 910  
 Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val  
 915 920 925  
 Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala  
 930 935 940  
 Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu  
 945 950 955 960  
 Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys  
 965 970 975  
 Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly  
 980 985 990  
 Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe  
 995 1000 1005  
 Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu  
 1010 1015 1020  
 Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile  
 1025 1030 1035 1040  
 Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro  
 1045 1050 1055  
 Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe  
 1060 1065 1070  
 Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser  
 1075 1080 1085  
 Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu  
 1090 1095 1100  
 Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg  
 1105 1110 1115 1120  
 Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg  
 1125 1130 1135  
 Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser  
 1140 1145 1150  
 Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg  
 1155 1160 1165  
 Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys  
 1170 1175 1180



Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala  
 1185 1190 1195 1200  
 Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu  
 1205 1210 1215  
 Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser  
 1220 1225 1230  
 Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro  
 1235 1240 1245  
 Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala  
 1250 1255 1260  
 His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro  
 1265 1270 1275 1280  
 Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His  
 1285 1290 1295  
 Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly  
 1300 1305 1310  
 Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro  
 1315 1320 1325  
 Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys  
 1330 1335 1340  
 Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu  
 1345 1350 1355 1360  
 Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala  
 1365 1370 1375  
 Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met  
 1380 1385 1390  
 Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu  
 1395 1400 1405  
 Pro Ser Glu Lys Ser Asp Glu Asp Asp Asp Lys Leu Asn Asp Ser Lys  
 1410 1415 1420  
 Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro  
 1425 1430 1435 1440  
 Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser  
 1445 1450 1455  
 Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg  
 1460 1465 1470  
 Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu  
 1475 1480 1485

Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile  
 1490 1495 1500  
 Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln  
 1505 1510 1515 1520  
 Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr  
 1525 1530 1535  
 Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys  
 1540 1545 1550  
 Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala  
 1555 1560 1565  
 Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn  
 1570 1575 1580  
 Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His  
 1585 1590 1595 1600  
 Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser  
 1605 1610 1615  
 Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn  
 1620 1625 1630  
 Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr  
 1635 1640 1645  
 Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg  
 1650 1655 1660  
 Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg  
 1665 1670 1675 1680  
 Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg  
 1685 1690 1695  
 Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu  
 1700 1705 1710  
 Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu  
 1715 1720 1725  
 Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Ser  
 1730 1735 1740  
 Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe  
 1745 1750 1755 1760  
 Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu  
 1765 1770 1775  
 Arg Asn Gly Arg Cys Leu Leu Leu Gln Gly Pro Gln His Cys Pro Phe  
 1780 1785 1790

Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Lys Val Val Leu Gly  
 1795 1800 1805  
 Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr  
 1810 1815 1820  
 Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe  
 1825 1830 1835 1840  
 Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys  
 1845 1850 1855  
 Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa  
 1860 1865 1870  
 Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro  
 1875 1880 1885  
 Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln  
 1890 1895 1900  
 Lys Thr Ile Lys Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys  
 1905 1910 1915 1920  
 Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp  
 1925 1930 1935  
 Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr  
 1940 1945 1950  
 Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn  
 1955 1960 1965  
 Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Leu Phe Tyr Trp Ile  
 1970 1975 1980  
 Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Phe Tyr  
 1985 1990 1995 2000  
 Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro  
 2005 2010 2015  
 Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg  
 2020 2025 2030  
 Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp  
 2035 2040 2045  
 Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val  
 2050 2055 2060  
 Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu  
 2065 2070 2075 2080  
 Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu  
 2085 2090 2095

Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr  
2100 2105

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1795 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe	Ala	Leu	Cys	Pro	Pro	Val	Thr	Gln	Arg	Glu	Pro	Gln	Glu	Thr	Arg	1	5	10	15
Glu	Cys	Arg	Lys	Phe	Ile	Phe	Glu	Ile	Leu	Ile	Phe	Glu	Glu	Ile	Cys	20	25	30	
Ile	His	Thr	His	Leu	Leu	Leu	Ile	Gly	Asp	Phe	Cys	Phe	Ile	Asn	Phe	35	40	45	
Leu	Ile	Phe	Thr	Met	Asn	Gly	His	Ser	Asp	Glu	Glu	Ser	Val	Arg	Asn	50	55	60	
Gly	Ser	Gly	Glu	Ser	Ser	Gln	Ser	Gly	Asp	Asp	Cys	Gly	Ser	Ala	Ser	65	70	75	80
Gly	Ser	Gly	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Asp	Gly	Ser	Ser	85	90	95	
Ser	Gln	Ser	Gly	Ser	Ser	Asp	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	100	105	110	
Gln	Ser	Glu	Ser	Glu	Ser	Asp	Thr	Ser	Arg	Glu	Asn	Lys	Val	Gln	Ala	115	120	125	
Lys	Pro	Pro	Lys	Val	Asp	Gly	Ala	Glu	Phe	Trp	Lys	Ser	Ser	Pro	Ser	130	135	140	
Ile	Leu	Ala	Val	Gln	Arg	Ser	Ala	Met	Leu	Arg	Lys	Gln	Pro	Gln	Gln	145	150	155	160
Ala	Gln	Gln	Gln	Arg	Pro	Ala	Ser	Ser	Asn	Ser	Gly	Ser	Glu	Glu	Asp	165	170	175	
Ser	Ser	Ser	Ser	Glu	Asp	Ser	Asp	Asp	Ser	Ser	Ser	Gly	Ala	Lys	Arg	180	185	190	
Lys	Lys	His	Asn	Asp	Glu	Asp	Trp	Gln	Met	Ser	Gly	Ser	Gly	Ser	Pro	195	200	205	

Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser  
 210 215 220  
 Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg  
 225 230 235 240  
 Ser Arg Lys Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile  
 245 250 255  
 Leu Gly Gln Lys Lys Arg Gln Ile Asp Ser Ser Glu Asp Glu Asp Asp  
 260 265 270  
 Glu Asp Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val  
 275 280 285  
 Asn Val Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp  
 290 295 300  
 Leu Leu Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Asp Glu Glu  
 305 310 315 320  
 Phe Glu Thr Ile Glu Arg Val Met Asp Cys Arg Val Gly Arg Lys Gly  
 325 330 335  
 Ala Thr Gly Ala Thr Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp  
 340 345 350  
 Pro Asn Ala Gly Phe Glu Arg Asn Lys Glu Pro Gly Asp Ile Gln Tyr  
 355 360 365  
 Leu Ile Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr  
 370 375 380  
 Glu Glu Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp  
 385 390 395 400  
 Asn Tyr Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala  
 405 410 415  
 Ser Pro Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp  
 420 425 430  
 Asp Leu His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser  
 435 440 445  
 Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln  
 450 455 460  
 Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser  
 465 470 475 480  
 Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser  
 485 490 495  
 Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg  
 500 505 510

Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly  
 515 520 525

Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His  
 530 535 540

Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu  
 545 550 555 560

Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu  
 565 570 575

His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu  
 580 585 590

Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala  
 595 600 605

Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His  
 610 615 620

Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu  
 625 630 635 640

Thr Thr Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu  
 645 650 655

Asn Trp Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp  
 660 665 670

Asp Ser Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg  
 675 680 685

Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp  
 690 695 700

Ser Leu Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp  
 705 710 715 720

Phe Glu Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu  
 725 730 735

His Lys Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val  
 740 745 750

Glu Lys Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met  
 755 760 765

Ser Ala Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr  
 770 775 780

Lys Ala Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn  
 785 790 795 800

Ile Met Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys  
 805 810 815

Pro Pro Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His  
 820 825 830  
 Leu Ile Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile  
 835 840 845  
 Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val  
 850 855 860  
 Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro  
 865 870 875 880  
 Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala  
 885 890 895  
 Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu  
 900 905 910  
 Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr  
 915 920 925  
 Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala  
 930 935 940  
 Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr  
 945 950 955 960  
 Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala  
 965 970 975  
 Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr  
 980 985 990  
 Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr  
 995 1000 1005  
 Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu  
 1010 1015 1020  
 Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met  
 1025 1030 1035 1040  
 Asp Ile Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro  
 1045 1050 1055  
 Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala  
 1060 1065 1070  
 Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg  
 1075 1080 1085  
 Asn Ser Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg  
 1090 1095 1100  
 Ile Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu  
 1105 1110 1115 1120

Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu  
 1125 1130 1135  
 Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser  
 1140 1145 1150  
 Ile Thr Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile  
 1155 1160 1165  
 Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe  
 1170 1175 1180  
 Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala  
 1185 1190 1195 1200  
 Val Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg  
 1205 1210 1215  
 Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp  
 1220 1225 1230  
 Asn Ser Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys  
 1235 1240 1245  
 Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val  
 1250 1255 1260  
 Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser  
 1265 1270 1275 1280  
 Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala  
 1285 1290 1295  
 Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu  
 1300 1305 1310  
 Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met  
 1315 1320 1325  
 Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp  
 1330 1335 1340  
 Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile  
 1345 1350 1355 1360  
 Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala  
 1365 1370 1375  
 Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys  
 1380 1385 1390  
 Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro  
 1395 1400 1405  
 Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys  
 1410 1415 1420



Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro  
 1425 1430 1435 1440  
 Leu Leu Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro  
 1445 1450 1455  
 Ile Ser Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys  
 1460 1465 1470  
 Lys Glu Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg  
 1475 1480 1485  
 Pro Glu Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln  
 1490 1495 1500  
 Cys Leu Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr  
 1505 1510 1515 1520  
 Thr Asn Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe  
 1525 1530 1535  
 Val Ser Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr  
 1540 1545 1550  
 Lys His Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln His Asn Asp Gln  
 1555 1560 1565  
 Asn Ile Ser Ser Asn Val Asn Thr His Val Ile Arg Asn Pro Asp Val  
 1570 1575 1580  
 Glu Arg Leu Lys Glu Thr Thr Asn His Asp Asp Ser Ser Arg Asp Ser  
 1585 1590 1595 1600  
 Tyr Ser Ser Asp Arg His Leu Ser Gln Tyr His Asp His His Lys Asp  
 1605 1610 1615  
 Arg His Gln Gly Asp Ala Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro  
 1620 1625 1630  
 Tyr Ser Ala Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr  
 1635 1640 1645  
 Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp  
 1650 1655 1660  
 Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys  
 1665 1670 1675 1680  
 Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile  
 1685 1690 1695  
 His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser  
 1700 1705 1710  
 Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser  
 1715 1720 1725

Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser  
1730 1735 1740

Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His  
1745 1750 1755 1760

Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg  
1765 1770 1775

Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His  
1780 1785 1790

Ser Asn Cys  
1795

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys Thr Xaa Glu Pro Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly  
1 5 10 15

Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln  
20 25 30

Gln Asn Val Arg Gly Met Lys Lys Leu Asp Asn Tyr Lys Lys Lys Asp  
35 40 45

Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro Glu Asp Val Glu  
50 55 60

Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu His Lys Gln Tyr  
65 70 75 80

Gln Ile Val Glu Arg Thr Asn Xaa Ser Phe Gln Ser Lys Ser Ala Ala  
85 90 95

Gly Tyr Pro

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 439 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile	Tyr	Arg	Leu	Val	Thr	Lys	Gly	Ser	Val	Glu	Glu	Asp	Ile	Leu	Glu	
1				5					10					15		
Arg	Ala	Lys	Lys	Lys	Met	Val	Leu	Asp	His	Leu	Val	Ile	Gln	Arg	Met	
			20					25					30			
Asp	Thr	Thr	Gly	Lys	Thr	Val	Leu	His	Thr	Gly	Ser	Thr	Pro	Ser	Ser	
			35				40					45				
Ser	Thr	Pro	Phe	Asn	Lys	Glu	Glu	Leu	Ser	Ala	Ile	Leu	Lys	Phe	Gly	
	50					55					60					
Ala	Glu	Glu	Leu	Phe	Lys	Glu	Pro	Glu	Xaa	Glu	Glu	Glu	Glu	Pro	Gln	
65					70					75					80	
Glu	Met	Asp	Ile	Asp	Glu	Ile	Leu	Lys	Arg	Xaa	Glu	Thr	Arg	Glu	Asn	
				85					90					95		
Glu	Ser	Gly	Pro	Leu	Thr	Val	Gly	Asp	Glu	Leu	Leu	Ser	Gln	Phe	Lys	
			100					105					110			
Val	Ala	Asn	Phe	Ser	Asn	Met	Asp	Glu	Asp	Asp	Ile	Glu	Leu	Glu	Pro	
		115					120					125				
Glu	Gln	Asn	Leu	Arg	Asn	Trp	Glu	Glu	Ile	Ile	Pro	Glu	Val	Gln	Trp	
		130				135					140					
Arg	Arg	Ile	Glu	Gly	Xaa	Glu	Arg	Gln	Lys	Glu	Leu	Glu	Glu	Ile	Tyr	
145					150					155					160	
Met	Leu	Pro	Arg	Met	Arg	Asn	Cys	Ala	Lys	Gln	Ile	Ser	Phe	Asn	Gly	
				165					170					175		
Asn	Glu	Gly	Arg	Cys	Ser	Arg	Ser	Arg	Arg	Tyr	Ser	Gly	Ser	Asp	Ser	
			180					185					190			
Asp	Ser	Ile	Ser	Glu	Arg	Lys	Arg	Pro	Lys	Lys	Arg	Gly	Arg	Pro	Arg	
		195					200					205				
Thr	Ile	Pro	Arg	Glu	Asn	Ile	Lys	Gly	Phe	Ser	Asp	Ala	Glu	Ile	Arg	
	210					215					220					
Arg	Phe	Ile	Lys	Ser	Tyr	Lys	Lys	Phe	Gly	Gly	Pro	Val	Glu	Arg	Leu	
225					230					235					240	
Asp	Ala	Ile	Ala	Arg	Asp	Ala	Glu	Leu	Val	Asp	Lys	Ser	Glu	Thr	Asp	
				245				250						255		

Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu  
 260 265 270  
 Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys  
 275 280 285  
 Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys  
 290 295 300  
 Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile  
 305 310 315 320  
 Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr  
 325 330 335  
 Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn  
 340 345 350  
 Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile  
 355 360 365  
 Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp  
 370 375 380  
 Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr  
 385 390 395 400  
 Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg  
 405 410 415  
 Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys  
 420 425 430  
 Asn Lys Ala Thr Lys Ala Ala  
 435

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..1434
- (D) OTHER INFORMATION: /note= "The sequence beginning at 1 corresponds to 55 and that ending at 1434 corresponds to 1488"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser  
 1 5 10 15  
 Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln Gln  
 20 25 30  
 Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser  
 35 40 45  
 Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys  
 50 55 60  
 His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly  
 65 70 75 80  
 Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys  
 85 90 95  
 Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg  
 100 105 110  
 Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly  
 115 120 125  
 Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Glu Asp Asp Asp  
 130 135 140  
 Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val  
 145 150 155 160  
 Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu  
 165 170 175  
 Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu  
 180 185 190  
 Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr  
 195 200 205  
 Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn  
 210 215 220  
 Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile  
 225 230 235 240  
 Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu  
 245 250 255  
 Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr  
 260 265 270  
 Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro  
 275 280 285  
 Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu  
 290 295 300

His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln  
 305 310 315 320  
 Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu  
 325 330 335  
 Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys  
 340 345 350  
 Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr  
 355 360 365  
 Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val  
 370 375 380  
 Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu  
 385 390 395 400  
 Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp  
 405 410 415  
 Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys  
 420 425 430  
 Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln  
 435 440 445  
 Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser  
 450 455 460  
 Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val  
 465 470 475 480  
 Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp  
 485 490 495  
 Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr  
 500 505 510  
 Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp  
 515 520 525  
 Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser  
 530 535 540  
 Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu  
 545 550 555 560  
 Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu  
 565 570 575  
 Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu  
 580 585 590  
 Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys  
 595 600 605

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys  
 610 615 620  
 Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala  
 625 630 635 640  
 Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala  
 645 650 655  
 Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met  
 660 665 670  
 Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro  
 675 680 685  
 Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile  
 690 695 700  
 Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu  
 705 710 715 720  
 Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met  
 725 730 735  
 Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln  
 740 745 750  
 Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp  
 755 760 765  
 His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr  
 770 775 780  
 Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val  
 785 790 795 800  
 Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala  
 805 810 815  
 Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu  
 820 825 830  
 Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys  
 835 840 845  
 Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly  
 850 855 860  
 Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr Pro Phe  
 865 870 875 880  
 Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu  
 885 890 895  
 Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile  
 900 905 910

Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro Gly Pro  
 915 920 925  
 Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe  
 930 935 940  
 Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser  
 945 950 955 960  
 Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg Ile Glu  
 965 970 975  
 Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg  
 980 985 990  
 Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg  
 995 1000 1005  
 Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Thr  
 1010 1015 1020  
 Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg  
 1025 1030 1035 1040  
 Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys  
 1045 1050 1055  
 Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala  
 1060 1065 1070  
 Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu  
 1075 1080 1085  
 Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser  
 1090 1095 1100  
 Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro  
 1105 1110 1115 1120  
 Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser  
 1125 1130 1135  
 His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro  
 1140 1145 1150  
 Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His  
 1155 1160 1165  
 Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly  
 1170 1175 1180  
 Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro  
 1185 1190 1195 1200  
 Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys  
 1205 1210 1215



Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu  
 1220 1225 1230  
 Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala Gly Ala  
 1235 1240 1245  
 Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys Met Lys  
 1250 1255 1260  
 Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Gln Pro  
 1265 1270 1275 1280  
 Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys Val Asn  
 1285 1290 1295  
 Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro Leu Leu  
 1300 1305 1310  
 Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro Ile Ser  
 1315 1320 1325  
 Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys Lys Glu  
 1330 1335 1340  
 Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu  
 1345 1350 1355 1360  
 Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu  
 1365 1370 1375  
 Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Thr Asn  
 1380 1385 1390  
 Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser  
 1395 1400 1405  
 Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His  
 1410 1415 1420  
 Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln  
 1425 1430

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..1467
- (D) OTHER INFORMATION:/note= "The sequence beginning at 1

corresponds to 2654 and that ending at 1467 corresponds to  
4120"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met	Ala	Ala	Lys	Asp	Ile	Ser	Thr	Glu	Val	Leu	Gln	Asn	Pro	Glu	Leu	1	5	10	15
Tyr	Gly	Leu	Arg	Arg	Ser	His	Arg	Ala	Ala	Ala	His	Gln	Gln	Asn	Tyr	20	25	30	
Phe	Asn	Asp	Ser	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Asn	Ile	Lys	Gln	Ser	35	40	45	
Arg	Arg	Lys	Arg	Met	Thr	Thr	Ile	Glu	Asp	Asp	Glu	Asp	Glu	Phe	Glu	50	55	60	
Asp	Glu	Glu	Gly	Glu	Glu	Asp	Ser	Gly	Glu	Asp	Glu	Asp	Glu	Glu	Asp	65	70	75	80
Phe	Glu	Glu	Asp	Asp	Asp	Tyr	Tyr	Gly	Ser	Pro	Ile	Lys	Gln	Asn	Arg	85	90	95	
Ser	Lys	Pro	Lys	Ser	Arg	Thr	Lys	Ser	Lys	Ser	Lys	Ser	Lys	Pro	Lys	100	105	110	
Ser	Gln	Ser	Glu	Lys	Gln	Ser	Thr	Val	Lys	Ile	Pro	Thr	Arg	Phe	Ser	115	120	125	
Asn	Arg	Gln	Asn	Lys	Thr	Val	Asn	Tyr	Asn	Ile	Asp	Tyr	Ser	Asp	Asp	130	135	140	
Asp	Leu	Leu	Glu	Ser	Glu	Asp	Asp	Tyr	Gly	Ser	Glu	Glu	Ala	Leu	Ser	145	150	155	160
Glu	Glu	Asn	Val	His	Glu	Ala	Ser	Ala	Asn	Pro	Gln	Pro	Glu	Asp	Phe	165	170	175	
His	Gly	Ile	Asp	Ile	Val	Ile	Asn	His	Arg	Leu	Lys	Thr	Ser	Leu	Glu	180	185	190	
Glu	Gly	Lys	Val	Leu	Glu	Lys	Thr	Val	Pro	Asp	Leu	Asn	Asn	Cys	Lys	195	200	205	
Glu	Asn	Tyr	Glu	Phe	Leu	Ile	Lys	Trp	Thr	Asp	Glu	Ser	His	Leu	His	210	215	220	
Asn	Thr	Trp	Glu	Thr	Tyr	Glu	Ser	Ile	Gly	Gln	Val	Arg	Gly	Leu	Lys	225	230	235	240
Arg	Leu	Asp	Asn	Tyr	Cys	Lys	Gln	Phe	Ile	Ile	Glu	Asp	Gln	Gln	Val	245	250	255	
Arg	Leu	Asp	Pro	Tyr	Val	Thr	Ala	Glu	Asp	Ile	Glu	Ile	Met	Asp	Met	260	265	270	

Glu Arg Glu Arg Arg Leu Asp Glu Phe Glu Glu Phe His Val Pro Glu  
 275 280 285  
 Arg Ile Ile Asp Ser Gln Arg Ala Ser Leu Glu Asp Gly Thr Ser Gln  
 290 295 300  
 Leu Gln Tyr Leu Val Lys Trp Arg Arg Leu Asn Tyr Asp Glu Ala Thr  
 305 310 315 320  
 Trp Glu Asn Ala Thr Asp Ile Val Lys Leu Ala Pro Glu Gln Val Lys  
 325 330 335  
 His Phe Gln Asn Arg Glu Asn Ser Lys Ile Leu Pro Gln Tyr Ser Ser  
 340 345 350  
 Asn Tyr Thr Ser Gln Arg Pro Arg Phe Glu Lys Leu Ser Val Gln Pro  
 355 360 365  
 Pro Phe Ile Lys Gly Gly Glu Leu Arg Asp Phe Gln Leu Thr Gly Ile  
 370 375 380  
 Asn Trp Met Ala Phe Leu Trp Ser Lys Gly Asp Asn Gly Ile Leu Ala  
 385 390 395 400  
 Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Val Ala Phe Ile Ser  
 405 410 415  
 Trp Leu Ile Phe Ala Arg Arg Gln Asn Gly Pro His Ile Ile Val Val  
 420 425 430  
 Pro Leu Ser Thr Met Pro Ala Trp Leu Asp Thr Phe Glu Lys Trp Ala  
 435 440 445  
 Pro Asp Leu Asn Cys Ile Cys Tyr Met Gly Asn Gln Lys Ser Arg Asp  
 450 455 460  
 Thr Ile Arg Glu Tyr Glu Phe Tyr Thr Asn Pro Arg Ala Lys Gly Lys  
 465 470 475 480  
 Lys Thr Met Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Leu  
 485 490 495  
 Lys Asp Arg Ala Glu Leu Gly Ser Ile Lys Trp Gln Phe Met Ala Val  
 500 505 510  
 Asp Glu Ala His Arg Leu Lys Asn Ala Glu Ser Ser Leu Tyr Glu Ser  
 515 520 525  
 Leu Asn Ser Phe Lys Val Ala Asn Arg Met Leu Ile Thr Gly Thr Pro  
 530 535 540  
 Leu Gln Asn Asn Ile Lys Glu Leu Ala Ala Leu Val Asn Phe Leu Met  
 545 550 555 560  
 Pro Gly Arg Phe Thr Ile Asp Gln Glu Ile Asp Phe Glu Asn Gln Asp  
 565 570 575

Glu Glu Gln Glu Glu Tyr Ile His Asp Leu His Arg Arg Ile Gln Pro  
 580 585 590  
 Phe Ile Leu Arg Arg Leu Lys Lys Asp Val Glu Lys Ser Leu Pro Ser  
 595 600 605  
 Lys Thr Glu Arg Ile Leu Arg Val Glu Leu Ser Asp Val Gln Thr Glu  
 610 615 620  
 Tyr Tyr Lys Asn Ile Leu Thr Lys Asn Tyr Ser Ala Leu Thr Ala Gly  
 625 630 635 640  
 Ala Lys Gly Gly His Phe Ser Leu Leu Asn Ile Met Asn Glu Leu Lys  
 645 650 655  
 Lys Ala Ser Asn His Pro Tyr Leu Phe Asp Asn Ala Glu Glu Arg Val  
 660 665 670  
 Leu Gln Lys Phe Gly Asp Gly Lys Met Thr Arg Glu Asn Val Leu Arg  
 675 680 685  
 Gly Leu Ile Met Ser Ser Gly Lys Met Val Leu Leu Asp Gln Leu Leu  
 690 695 700  
 Thr Arg Leu Lys Lys Asp Gly His Arg Val Leu Ile Phe Ser Gln Met  
 705 710 715 720  
 Val Arg Met Leu Asp Ile Leu Gly Asp Tyr Leu Ser Ile Lys Gly Ile  
 725 730 735  
 Asn Phe Gln Arg Leu Asp Gly Thr Val Pro Ser Ala Gln Arg Arg Ile  
 740 745 750  
 Ser Ile Asp His Phe Asn Ser Pro Asp Ser Asn Asp Phe Val Phe Leu  
 755 760 765  
 Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Met Thr Ala Asp  
 770 775 780  
 Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Ala Asp Leu Gln  
 785 790 795 800  
 Ala Met Ala Arg Ala His Arg Ile Gly Gln Lys Asn His Val Met Val  
 805 810 815  
 Tyr Arg Leu Val Ser Lys Asp Thr Val Glu Glu Glu Val Leu Glu Arg  
 820 825 830  
 Ala Arg Lys Lys Met Ile Leu Glu Tyr Ala Ile Ile Ser Leu Gly Val  
 835 840 845  
 Thr Asp Gly Asn Lys Tyr Thr Lys Lys Asn Glu Pro Asn Ala Gly Glu  
 850 855 860  
 Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr  
 865 870 875 880

Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn  
 885 890 895  
 His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu  
 900 905 910  
 Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala  
 915 920 925  
 Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Glu Leu Lys Lys Leu  
 930 935 940  
 Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln  
 945 950 955 960  
 Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn  
 965 970 975  
 Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp  
 980 985 990  
 Ser Thr Ser Arg Ser Ser Arg Arg Arg Ala Arg Ala Asn Asp Met Asp  
 995 1000 1005  
 Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys  
 1010 1015 1020  
 Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr  
 1025 1030 1035 1040  
 Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met  
 1045 1050 1055  
 Met Glu Ala Ala Lys Asp Cys Val His Glu Glu Glu Lys Asn Arg Lys  
 1060 1065 1070  
 Glu Ile Leu Glu Lys Leu Glu Lys His Ala Thr Ala Tyr Arg Ala Lys  
 1075 1080 1085  
 Leu Lys Ser Gly Glu Ile Lys Ala Glu Asn Gln Pro Lys Asp Asn Pro  
 1090 1095 1100  
 Leu Thr Arg Leu Ser Leu Lys Lys Arg Glu Lys Lys Ala Val Leu Phe  
 1105 1110 1115 1120  
 Asn Phe Lys Gly Val Lys Ser Leu Asn Ala Glu Ser Leu Leu Ser Arg  
 1125 1130 1135  
 Val Glu Asp Leu Lys Tyr Leu Lys Asn Leu Ile Asn Ser Asn Tyr Lys  
 1140 1145 1150  
 Asp Asp Pro Leu Lys Phe Ser Leu Gly Asn Asn Thr Pro Lys Pro Val  
 1155 1160 1165  
 Gln Asn Trp Ser Ser Asn Trp Thr Lys Glu Glu Asp Glu Lys Leu Leu  
 1170 1175 1180

Ile Gly Val Phe Lys Tyr Gly Tyr Gly Ser Trp Thr Gln Ile Arg Asp  
 1185 1190 1195 1200  
 Asp Pro Phe Leu Gly Ile Thr Asp Lys Ile Phe Leu Asn Glu Val His  
 1205 1210 1215  
 Asn Pro Val Ala Lys Lys Ser Ala Ser Ser Ser Asp Thr Thr Pro Thr  
 1220 1225 1230  
 Pro Ser Lys Lys Gly Lys Gly Ile Thr Gly Ser Ser Lys Lys Val Pro  
 1235 1240 1245  
 Gly Ala Ile His Leu Gly Arg Arg Val Asp Tyr Leu Leu Ser Phe Leu  
 1250 1255 1260  
 Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys  
 1265 1270 1275 1280  
 Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn  
 1285 1290 1295  
 His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn  
 1300 1305 1310  
 Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala  
 1315 1320 1325  
 Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu  
 1330 1335 1340  
 Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro  
 1345 1350 1355 1360  
 Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu  
 1365 1370 1375  
 Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu  
 1380 1385 1390  
 Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu  
 1395 1400 1405  
 Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly  
 1410 1415 1420  
 Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser  
 1425 1430 1435 1440  
 Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met  
 1445 1450 1455  
 Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys  
 1460 1465

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Lys Ser Lys
1           5           10           15

Glu Leu Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His
          20           25           30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val
          35           40           45

Lys Gly Met Asn Lys Leu Asp Asn Tyr Lys Lys
          50           55

```

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Arg Asn Lys
1           5           10           15

Glu Pro Gly Asp Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His
          20           25           30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val
          35           40           45

Arg Gly Asn Lys Lys Leu Asp Asn Tyr Lys Lys
          50           55

```

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys  
1 5 10 15

Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His  
20 25 30

Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys  
35 40 45

Arg Leu Asp Asn Tyr Cys Lys  
50 55

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu Glu Glu Glu Glu Tyr Ala Val Glu Lys Ile Ile Asp Arg Arg Val  
1 5 10 15

Arg Lys Gly Lys Val Glu Tyr Tyr Leu Lys Trp Lys Gly Tyr Pro Glu  
20 25 30

Thr Glu Asn Thr Trp Glu Pro Glu Asn Asn Leu Asp Cys Gln Asp Leu  
35 40 45

Ile Gln Gln Tyr  
50

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val  
1 5 10 15  
Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser  
20 25 30  
Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu  
35 40 45  
Leu Ile Ser Glu Phe  
50

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val  
1 5 10 15  
Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp  
20 25 30  
Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu  
35 40 45  
Ile Ala Glu Phe  
50

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val  
1 5 10 15  
Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp  
20 25 30  
Ala Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Glu Leu  
35 40 45  
Ile Glu Asp Phe  
50

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro Val Asp Leu Val Tyr Ala Ala Glu Lys Ile Ile Gln Lys Arg Val  
1 5 10 15  
Lys Lys Gly Val Val Glu Tyr Arg Val Lys Trp Lys Gly Trp Asn Gln  
20 25 30  
Arg Tyr Asn Thr Trp Glu Pro Glu Asn Asn Ile Leu Asp Arg Arg Leu  
35 40 45  
Ile Asp Ile Tyr  
50

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu  
 1 5 10 15  
 Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser  
 20 25 30  
 Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu  
 35 40 45  
 Leu Leu Ala Phe  
 50

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG 60  
 CGACCCCGCA CTATCCCTCG GGAGAATATT AAAGGATTTA GTGATGCGGA G 111

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGAATCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGGA 60  
 AGACCTCGAA CCATTCCTCG AGAAAATATT AAAGGATTTA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCCAAAAAA GCGTGGAAGA CCACGAATA TTCCTCGAGA 60  
AAATATA 67

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAA AAAACGTGGA 60  
CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTTA GTGATGCAGA G 111

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAATA TTCCTCGTGA 60  
AAATATT 67

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGACTCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA 60  
CTATCCCTCG GGAGAATATT AAAGGATTTA GCGATGCAGA GATTAGGCGG T 111

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC 24

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA 23

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Lys Arg Pro Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Arg Gly Arg Pro Arg  
1 5